

SEQUENCE LISTING

<110> Ni et al.

<120> T1-R Ligand III

<130> PF357C1

<150> 09/030,847

<151> 1998-02-26

<150> 60/039,483

<151> 1997-02-28

<160> 16

<170> PatentIn version 3.1

<210> 1

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<212> DNA

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<222> (103)..(519)

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ggg tgc agg ctg ctc gca ctg ctg cta ctg gtg cct gga ccc ggc ggc 102
Gly Cys Arg Leu Leu Ala Leu Leu Leu Val Pro Gly Pro Gly Gly
-15 -10 -5 -1

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Ala Ser Glu Ile Thr Phe Glu Leu Pro Asp Asn Ala Lys Gln Cys Phe
1 5 10 15

tac gag gac atc gct cag ggc acc aag tgc acc ctg gag ttc cag gtg 198
Tyr Glu Asp Ile Ala Gln Gly Thr Lys Cys Thr Leu Glu Phe Gln Val
20 25 30

att act ggt ggt cac tat gat gta gat tgt cga tta gaa gat cct gat 246
Ile Thr Gly Gly His Tyr Asp Val Asp Cys Arg Leu Glu Asp Pro Asp
35 40 45

ggt aaa gtg tta tac aaa gag atg aag aaa cag tat gat agt ttt acc 294
 Gly Lys Val Leu Tyr Lys Glu Met Lys Lys Gln Tyr Asp Ser Phe Thr
 50 55 60

ttc aca gcc tcc aaa aat ggg aca tac aaa ttt tgc ttc agc aat gaa 342
 Phe Thr Ala Ser Lys Asn Gly Thr Tyr Lys Phe Cys Phe Ser Asn Glu
 65 70 75 80

ttt tct act ttc aca cat aaa act gta tat ttt gat ttt caa gtt gga 390
 Phe Ser Thr Phe Thr His Lys Thr Val Tyr Phe Asp Phe Gln Val Gly
 85 90 95

gaa gac cca cct ttg ttt cct agt gag aac cga gtc agt gct ctt acc 438
 Glu Asp Pro Pro Leu Phe Pro Ser Glu Asn Arg Val Ser Ala Leu Thr
 100 105 110

cag gta aat aaa aaa atc agc aat ata atg ttg gta tat tta aaa gga 486
 Gln Val Asn Lys Lys Ile Ser Asn Ile Met Leu Val Tyr Leu Lys Gly
 115 120 125

gga aaa aag cat aat tta ata tca tgc act aac tga tgagcatgga 532
 Gly Lys Lys His Asn Leu Ile Ser Cys Thr Asn
 130 135

attttgagac tgacagtctt taaaatctat cttaattctt acatgtaggc atttcacaga 592
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 cttggccaaa gtcatggtga aagaaacagc tttagaatg tgtaaaagcc ttaattcata 1552
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 Cys Arg Leu Leu Ala Leu Leu Leu Leu Val Pro Gly Pro Gly Gly Ala
 -15 -10 -5 -1 1

tct gag atc acc ttc gag ctt cct gac aac gcc aag cag tgc ttc tac 150
 Ser Glu Ile Thr Phe Glu Leu Pro Asp Asn Ala Lys Gln Cys Phe Tyr
 5 10 15

gag gac atc gct cag ggc acc aag tgc acc ctg gag ttc cag gtg att 198
 Glu Asp Ile Ala Gln Gly Thr Lys Cys Thr Leu Glu Phe Gln Val Ile
 20 25 30

act ggt ggt cac tat gat gta gat tgt cga tta gaa gat cct gat ggt 246
 Thr Gly Gly His Tyr Asp Val Asp Cys Arg Leu Glu Asp Pro Asp Gly
 35 40 45

aaa gtg tta tac aaa gag atg aag aaa cag tat gat agt ttt acc ttc 294
 Lys Val Leu Tyr Lys Glu Met Lys Lys Gln Tyr Asp Ser Phe Thr Phe
 50 55 60 65

aca gcc tcc aaa aat ggg aca tac aaa ttt tgc ttc agc aat gaa ttt 342
 Thr Ala Ser Lys Asn Gly Thr Tyr Lys Phe Cys Phe Ser Asn Glu Phe
 70 75 80

tct act ttc aca cat aaa act gta tat ttt gat ttt caa gtt gga gaa 390
 Ser Thr Phe Thr His Lys Thr Val Tyr Phe Asp Phe Gln Val Gly Glu
 85 90 95

gac cca cct ttg ttt cct agt gag aac cga gtc agt gct ctt acc cag 438
 Asp Pro Pro Leu Phe Pro Ser Glu Asn Arg Val Ser Ala Leu Thr Gln
 100 105 110

atg gaa tct gcc tgt gtt tca att cac gaa gct ctg aag tct gtc atc 486
 Met Glu Ser Ala Cys Val Ser Ile His Glu Ala Leu Lys Ser Val Ile
 115 120 125

gat tat cag act cat ttc cgt tta aga gaa gct caa ggc cga agc cga 534
 Asp Tyr Gln Thr His Phe Arg Leu Arg Glu Ala Gln Gly Arg Ser Arg
 130 135 140 145

gca gag gat cta aat aca aga gtg gcc tat tgg tca gta gga gaa gcc 582
 Ala Glu Asp Leu Asn Thr Arg Val Ala Tyr Trp Ser Val Gly Glu Ala
 150 155 160

ctc att ctt ctg gtg gtt agc ata ggg cag gta ttt ctt ttg aaa agc 630
 Leu Ile Leu Leu Val Val Ser Ile Gly Gln Val Phe Leu Leu Lys Ser
 165 170 175

ttt ttc tca gat aaa aga acc acc aca act cgt gtt gga tca 672
 Phe Phe Ser Asp Lys Arg Thr Thr Thr Arg Val Gly Ser
 180 185 190

taactacgtt ttgagaattg atgcaccatt gccactgtaa tattgctgtc ctctaattaa 732
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 Leu Leu Val Pro Gly Pro Gly Gly Ala Ser Glu Ile Thr Phe Glu Leu
 -5 -1 1 5
 Pro Asp Asn Ala Lys Gln Cys Phe Tyr Glu Asp Ile Ala Gln Gly Thr
 10 15 20
 Lys Cys Thr Leu Glu Phe Gln Val Ile Thr Gly Gly His Tyr Asp Val
 25 30 35 40

Asp Cys Arg Leu Glu Asp Pro Asp Gly Lys Val Leu Tyr Lys Glu Met
 45 50 55
 Lys Lys Gln Tyr Asp Ser Phe Thr Phe Thr Ala Ser Lys Asn Gly Thr
 60 65 70
 Tyr Lys Phe Cys Phe Ser Asn Glu Phe Ser Thr Phe Thr His Lys Thr
 75 80 85
 Val Tyr Phe Asp Phe Gln Val Gly Glu Asp Pro Pro Leu Phe Pro Ser
 90 95 100
 Glu Asn Arg Val Ser Ala Leu Thr Gln Met Glu Ser Ala Cys Val Ser
 105 110 115 120
 Ile His Glu Ala Leu Lys Ser Val Ile Asp Tyr Gln Thr His Phe Arg
 125 130 135
 Leu Arg Glu Ala Gln Gly Arg Ser Arg Ala Glu Asp Leu Asn Thr Arg
 140 145 150
 Val Ala Tyr Trp Ser Val Gly Glu Ala Leu Ile Leu Leu Val Val Ser
 155 160 165
 Ile Gly Gln Val Phe Leu Leu Lys Ser Phe Phe Ser Asp Lys Arg Thr
 170 175 180
 Thr Thr Thr Arg Val Gly Ser
 185 190

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 35 40 45
 Ser Ala Pro Ala Asn Ala Ser Leu Glu Thr Glu Tyr Gln Val Ile Gly
 50 55 60
 Gly Ala Gly Leu Asp Val Asp Phe Thr Leu Glu Ser Pro Gln Gly Val
 65 70 75 80
 Leu Leu Val Ser Glu Ser Arg Lys Ala Asp Gly Val His Thr Val Glu
 85 90 95
 Pro Thr Glu Ala Gly Asp Tyr Lys Leu Cys Phe Asp Asn Ser Phe Ser
 100 105 110

Thr Ile Ser Glu Lys Leu Val Phe Phe Glu Leu Ile Phe Asp Ser Leu
 115 120 125
 Gln Asp Asp Glu Glu Val Glu Gly Trp Ala Glu Ala Val Glu Pro Glu
 130 135 140
 Glu Met Leu Asp Val Lys Met Glu Asp Ile Lys Glu Ser Ile Glu Thr
 145 150 155 160
 Met Arg Thr Arg Leu Glu Arg Ser Ile Gln Met Leu Thr Leu Leu Arg
 165 170 175
 Ala Phe Glu Ala Arg Asp Arg Asn Leu Gln Glu Gly Asn Leu Glu Arg
 180 185 190
 Val Asn Phe Trp Ser Ala Val Asn Val Ala Val Leu Leu Leu Val Ala
 195 200 205
 Val Leu Gln Val Cys Thr Leu Lys Arg Phe Phe Gln Asp Lys Arg Pro
 210 215 220
 Val Pro Thr
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 cctggacaac gcaagcagtg cttctacgag gacatcgctc agggcaccaa gtgcaccctg 180
 ggagttccag tgattactgg tggtcactga tatgtagatt gtcgattaga agatcctgat 240
 ggtaaaagtgt tatacaaaga gattagtaac agttggtaat ttttacctta cagcttccaa 300
 aaagggggac at 312

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 gaaccgagta gtgctcttac ccagatggaa tcgcctgtgt ttcaattcac gaggctctga 120

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 taggtactga agaacttaat attggcaaca tttttaaatc cttactcata cacttggttg 180
 gagggatgta caatgcatat tcccaaactg tggaaaggac accttttttt atttgtaaag 240
 gtggaaaact ttggaactca ttttgggcta ttcattgtaa atattcaaca ccaatgatct 300
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 aaccttt 367

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 cacacataag tgccatacat tttatcctca tggatgtgat gcactgaaaa gttagttgct 180
 ctcttttttt cttttttttg tcgtgcatat tttatttctg tagtttctgg ttagctaccc 240
 taaagtgatt taaaaattta gaatgctttg tgtttcctat ttggtaatct tcattgactt 300
 ttcttttagtt aatgagtatt aaatgggtgca taccctgtag actatagggt tacaatgggt 360
 gcaccttata acttggatta gatggcgatt gaatagggtt ggtcccagtt tatccgttgg 420
 atccaagtgg ttccaaattt ttggtttaag gcttcgcggy ttttttttta gcaccgtttt 480
 ccgggccttc ccccaa 496

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<210> 12
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 <213> Artificial sequence

<220>
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<400> 12
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<210> 13
 <211> 38
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Contains a BamHI restriction site

<400> 13
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<210> 14
 <211> 27
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Contains an Asp718 restriction site

<400> 14
 cgcggtaccg aaatgcctac atgtaag 27

<210> 15
 <211> 27
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Contains an Asp718 restriction site

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<210> 16
 <211> 24
 <212> DNA
 <213> Artificial sequence

<220>

<223> Synthetic oligonucleotide probe containing an NF-kappa B
enhancer element

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24